JJBS
Jordan Journal of Biological Sciences

Volume 8, Number 3, September .2015
ISSN 1995-6673
Pages 175 - 181

Inheritance Pattern of Metric Characters Affecting Grain Yield in Two Bread Wheat (*Triticum aestivum* L.) Crosses Under Rainfed Conditions

Zine El Abidine Fellahi [1, 2, *], Abderrahmane Hannachi [2], Hamenna Bouzerzour [3] and Abdelkader Benbelkacem [4]

[1] *Agronomy Department, Faculty of Life and Natural Sciences, Ferhat Abbas University, Setif 1,* ***Al****geria.*

[2] *Algerian National Institute of Agronomic Research (INRAA), Research Unit of Setif, Algeria.*

[3] *Ecology and Biology Department, Faculty of Life and Natural Sciences, LVRBN Laboratory, Ferhat Abbas University, Setif 1, Algeria.*

[4] *Algerian National Institute of Agronomic Research (INRAA), Research Unit of Constantine, Algeria.*

Received: March 5, 2015 Revised: March 21 , 2015 Accepted: March 31, 2015

Abstract

The present investigation was undertaken to study the inheritance pattern and genetic analysis of some indicators of grain yield in F_1 and F_2 populations of two bread wheat crosses. The results reflected a satisfactory range of variability within and among the studied generations. Significant positive selection differentials were observed for all characters. High heritability estimates, coupled with high to moderate expected response to selection, were observed in most traits. High predicted genetic gain was observed for grain yield and above ground biomass. The estimated number of genes, involved in the genetic control of these characteristics, varied between 2 to 5, showing partial to over-dominance, suggesting that the selection must therefore be delayed until the F_4 or F_5 generation. Significant heterotic values in positive direction were found for all characters except thousand-kernel weight in both crosses and number of grains per spike in Acsad_{899} × Mahon-Demias cross. Inbreeding depression was observed in both crosses for the number of spikes, above-ground biomass and grain yield. The obtained results indicated that the studied crosses would be of interest in the breeding program. It was suggested that the selection for all characters, except for thousand-kernel weight, should be effective in early segregating generations due to additive gene effects.

Keywords: Heritability, Heterosis, Potence ratio, Semi-arid, Wheat, Yield.

1. Introduction

In Algeria, bread wheat (*Triticum aestivum* L.) is one of the most important food crops. It is mainly grown in the northern part of the country under rain fed conditions (Fellahi *et al*., 2013), where the production is subject to the fluctuation in the total yearly precipitation in addition to its distribution over the crop cycle (Chennafi *et al*., 2006). Drought is a major limiting factor of cereal crops production, posing a serious threat to food security worldwide (Cattivelli *et al.,* 2008). Water deficit is a multidimensional stress affecting plants at various levels of their organization (Blum, 1996). When subjected to water deficit, wheat demonstrates various morphological, physiological, biochemical, and molecular adaptive responses (Nezhadahmadi *et al*., 2013). During the post-anthesis stage, drought reduces plant size, leaf area, grain filling duration, grain number, thousand-kernel weight and grain yield (Kaur and Behl, 2010; Nouri *et al*., 2011). Physiological responses to water stress include stomata closure, development of oxidative stress, decrease in photosynthesis activity, alteration of the integrity of cell wall, production of metabolites to toxic levels, which cause plant death (Bray, 2002).

The genetic improvement of drought tolerance is an important objective in wheat breeding programs, in arid and semi-arid regions (Mullet and Whitsitt, 1996). Plant breeders need to develop varieties which are resilient to moisture stress conditions and able to express high grain

---

[*] Corresponding author. e-mail: zinou.agro@gmail.com.

yield potential (Noorka *et al.*, 2009). This requires a search for and a selection of traits such as biological yield, thousand-kernel weight, number of spikes, number of grains per spike and harvest index, which were found to be highly associated with grain yield (Richards *et al.*, 2002). Increasing the genetic potential of these traits is a continuous process. To accumulate a desirable gene pool in improved varieties, it is necessary to understand the mode of inheritance, the magnitude of gene effect and the mode of gene action in relation to the targeted environment for which varieties are to be developed (Farshadfar *et al.*, 2000). Previous genetic studies reported that both additive and non-additive gene actions were involved in the expression of most agronomic characters (Hannachi *et al.*, 2013). Nevertheless, the selection of promising parents to obtain superior hybrids depends, primarily, on the predominance of additive effect (Gowda *et al.*, 2010; Beche *et al.*, 2013). Keeping in view the importance of some metric characters as grain yield determinants under rain fed growth conditions, the goal of this research was to investigate the inheritance pattern of these metric traits in two bread wheat (*Triticum aestivum* L.) crosses utilizing P_1, P_2, F_1 and F_2 populations data sets.

2. Materials and Methods

2.1. Experimental Material and Design

The experience was carried out at the experimental field of the Algerian National Institute of Agronomic Research (INRAA), unit of Setif, during three successive crop seasons: 2010/11, 2011/12 and 2012/13. The experimental site coordinates are 36°15′N, 05°37′E and 981 m above sea level. In the 2010/11 cropping season, four genotypes Acsad_{899}, Mahon-Demias, Acsad_{1069} and Rmada were crossed to obtain F_1 seeds of the following crosses Acsad_{899} × Mahon-Demias and Acsad_{1069} × Rmada. In the second season, the hybrid seeds of the two crosses were sown to grow the F_1 plants, which were selfed to produce F_2 seeds.

During the third season, seeds of four populations, P_1, P_2, F_1 and F_2, of each of the two crosses were sown in a randomized complete block design, with three replications. Plot had two rows of 10 m length, spaced 20 cm apart, with a plant to plant distance maintained at 10 cm by appropriate plant thinning. Ten competitive plants from parents, F_1 and thirty plants from F_2 generations were randomly harvested from each replication and measurements of above-ground biomass, thousand-kernel weight, spike number, number of grains per spike and grain yield were made.

2.2. Statistical Analysis and Estimation of Genetic Parameters

2.2.1. Variance Components, Heritability and Minimum Number of Genes

Estimates of phenotypic (σ^2_p), genotypic (σ^2_g) and environmental (σ^2_e) variances were obtained from the data of the parents and their offspring generations according to the method outlined by Cruz *et al.* (2012). Broad sense heritability (h^2_{bs}) was calculated using the components of variance derived from the parental and the offspring generations' data according to Acquaah (2007).

$$h_{bs}{}^2(\%) = \frac{\sigma^2{}_g}{\sigma^2{}_p} \times 100$$

where, σ^2_g = genotypic variance, σ^2_p = phenotypic variance.

The minimum number of genes involved in the control of each trait was estimated according to Burton (1951).

2.2.2. Selection Differential and Expected Response to Selection

Selection differential (*S*), the expected response to selection (*RS*), the expected response to selection expressed as % of the base population mean (*%RS*) and the expected genetic gain (*PGG*) were calculated using the formulas reported by Cruz *et al.* (2012).

$$S = (\bar{X}_s - \bar{X}_o)$$

$$RS = S \times h^2{}_{ns}$$

$$RS\ (\%) = 100 \times (\frac{RS}{\bar{X}_o})$$

$$PGG = (\bar{X}_o + RS)$$

2.2.3. Heterosis, potence ratio and inbreeding depression

The percent increase or decrease of F_1 hybrids over mid parent value was calculated to estimate heterosis, following Fonsecca and Patterson (1968). The dominance estimate (*P*) was determined using the potence ratio method (Peter and Frey, 1966). Inbreeding depression (*ID*) was estimated by calculating the percent decrease of F_2 population mean over F_1 hybrid mean:

$$Heterosis = 100 \times \left(\frac{\bar{X}F1 - \bar{X}MP}{\bar{X}MP}\right)$$

$$P = 2 \times \left(\frac{\bar{X}F1 - \bar{X}MP}{\bar{X}BP - \bar{X}MP}\right)$$

$$ID\ (\%) = 100 \times \left(\frac{\bar{X}F1 - \bar{X}F2}{\bar{X}F1}\right)$$

where $\bar{X}_{F1}$ = the first generation mean, $\bar{X}_{F2}$ = the second generation mean, $\bar{X}_{MP}$ = mid parent mean, $\bar{X}_{BP}$ = best parent mean. All statistical analyses were carried out using Genes software (Cruz, 2013) and Microsoft Excel spreadsheets.

3. Results

3.1. Mean Performances of the Evaluated Populations

Means and variances for the analyzed traits of the two crosses are presented in Table 1. Parents showed difference for all traits, in both crosses, except for thousand-kernel weight in Acsad_{1069} × Rmada cross. Mean values of the first filial generation of the Acsad_{899} × Mahon-Demias cross were between parental values for the number of grains per spike. In both crosses, the performances of F_1's were better than those of the best parents for the number of spikes per plant, above-ground biomass and grain yield. However, the F_1 mean performance of the number of grains per spike was higher than that of the best parent in Acsad_{1069} × Rmada cross only. Furthermore, F_1 generation showed significant decline over respective parent for thousand-kernel weight in both crosses. These results indicated the presence of heterotic effects for these characters. Means of the second filial generations were between parental values for thousand-kernel weight, number of grains per spike, biomass per plant and grain yield in Acsad$_{899}$ × Mahon cross. F$_2$ population mean exceeded the mean of the best parent for number of spikes per plant in both crosses and for thousand-kernel weight, above-ground biomass per plant and grain yield in Acsad$_{1069}$ × Rmada cross. These results indicated the presence of transgressive segregants in the F$_2$ generation for number of spikes per plant and thousand-kernel weight. Both traits are important determinants of grain yield, under semi-arid conditions. In addition, F$_2$ generation, of Acsad$_{1069}$ × Rmada cross exhibited lower number of grains per spike than the lowest parent. The largest variances for all evaluated traits were found in the F$_2$ generation. These results were somewhat expected, since the observed variability of the F$_2$ generation is due to environmental and genetic sources (Falconer and MacKay, 1996).

Table 1. Means ($\bar{X}$) and variances (σ^2) for the studied characters of four wheat populations (P$_1$, P$_2$, F$_1$ and F$_2$) derived from two bread wheat crosses.

Generation	Parameter	Characters				
		TKW	NS	NGS	BIO	GY
Acsad$_{899}$ × Mahon-Demias						
P$_1$	$\bar{X}$	39.47	5.87	48.82	24.00	11.41
	σ^2	17.78	4.88	150.48	105.24	33.32
P$_2$	$\bar{X}$	40.79	9.23	33.77	33.40	12.77
	σ^2	2.06	9.21	60.48	173.21	26.51
F$_1$	$\bar{X}$	33.11	17.67	35.07	56.93	20.40
	σ^2	1.14	10.33	3.70	82.97	9.12
F$_2$	$\bar{X}$	36.27	9.80	35.01	31.97	12.72
	σ^2	22.02	22.71	108.90	279.82	64.49
Acsad$_{1069}$ × Rmada						
P$_1$	$\bar{X}$	34.58	5.50	49.34	22.29	9.58
	σ^2	4.81	3.43	214.82	126.99	25.70
P$_2$	$\bar{X}$	34.69	7.40	48.97	24.17	12.40
	σ^2	5.25	10.52	146.67	107.87	35.90
F$_1$	$\bar{X}$	29.87	14.00	53.04	54.73	22.18
	σ^2	4.55	3.00	5.97	46.97	12.20
F$_2$	$\bar{X}$	37.20	8.00	44.60	30.37	13.81
	σ^2	18.66	11.66	199.02	274.79	59.80

TKW: Thousand-kernel weight (g), NS: Number of spikes per plant, NGS: Number of grains per spike, BIO: Biomass per plant (g), GY: Grain yield per plant (g).

3.2. Variance Components, Heritability and Minimum Number of Genes

Estimates of the components of variance, heritability, potence ratio and the minimum number of genes are presented in Table 2. In the present study, the values of the components of genetic variance were generally greater than the environmental component of variance for all traits except the number of grains per spike in Acsad$_{899}$ × Mahon-Demias, where the two components are of similar magnitude (Table 2). Therefore, the observed phenotypic variance can be associated, in most part, to the effect of their genetic differences, with negligible environmental effects. Contributions of genotypic variance to the total variance, in Acsad$_{899}$ × Mahon-Demias cross, were 74.9, 61.7, 49.9, 60.3 and 69.7 % for thousand-kernel weight, number of spikes per plant, number of grains per spike, above ground biomass and grain yield, respectively (Figure 1). These figures were 74.3, 57.2, 53.1, 70.1 and 64.0 % in Acsad$_{1069}$ × Rmada cross for the above mentioned traits (Figure 1). In the present study, estimates of broad sense heritability ranged between 49.87 and 74.88 % (Table 2). Both low and high h^2_{bs} values were observed in Acsad$_{899}$ × Mahon-Demias cross for the number of grains per spike and thousand-kernel weight, respectively. Generally, values of broad sense heritability were either equal to or greater than 50% for all characters understudy, indicating possibilities for improvement through selection in the genetic material produced.

The minimum number of genes is a useful indicator of the polygenic nature of the character studied. The minimum number of genes controlling thousand-kernel weight, spikes number, number of grains per spike, above ground biomass and grain yield in Acsad$_{899}$ × Mahon-Demias cross were 3.48, 2.90, 2.75, 4.86 and 4.85, respectively (Table 2). In the Acsad$_{1069}$ × Rmada cross, these figures were 2.24, 4.21, 5.39, 2.82 and 3.47, respectively. These results indicated that the characters under study are controlled by a relatively small number of genes and a few selection cycles would be necessary to obtain the required accumulation of the favorable alleles controlling them.

Table 2. Estimates of phenotypic (σ_p^2), genotypic (σ_g^2) and environmental (σ_e^2) variance components, broad sense heritability (h^2_{bs}), and minimum number of genes (mng) for the studied characters of four populations (P$_1$, P$_2$, F$_1$ and F$_2$) derived from two bread wheat crosses.

Genetic component	Characters				
	TKW	NS	NGS	BIO	GY
Acsad$_{899}$ × Mahon-Demias					
σ_p^2	22.02	22.71	108.90	279.82	64.49
σ_g^2	16.49	14.02	54.31	168.72	44.97
σ_e^2	5.53	8.69	54.59	111.10	19.52
h^2_{bs} (%)	74.88	61.74	49.87	60.30	69.72
F$_2$ range	23.81/45.26	4.00/22.00	20.91/55.49	11.00/92.00	2.08/43.85
mng	3.48	2.90	2.75	4.86	4.85
Acsad$_{1069}$ × Rmada					
σ_p^2	18.66	11.66	199.02	274.79	59.80
σ_g^2	13.87	6.67	105.67	192.59	38.30
σ_e^2	4.79	4.99	93.36	82.20	21.50
h^2_{bs} (%)	74.30	57.20	53.09	70.09	64.05
F$_2$ range	29.67/45.44	4.00/19.00	13.34/80.87	9.00/75.00	2.37/34.99
mng	2.24	4.21	5.39	2.82	3.47

TKW: Thousand-kernel weight (g), NS: Number of spikes per plant, NGS: Number of grains per spike, BIO: Biomass per plant (g), GY: Grain yield per plant (g).

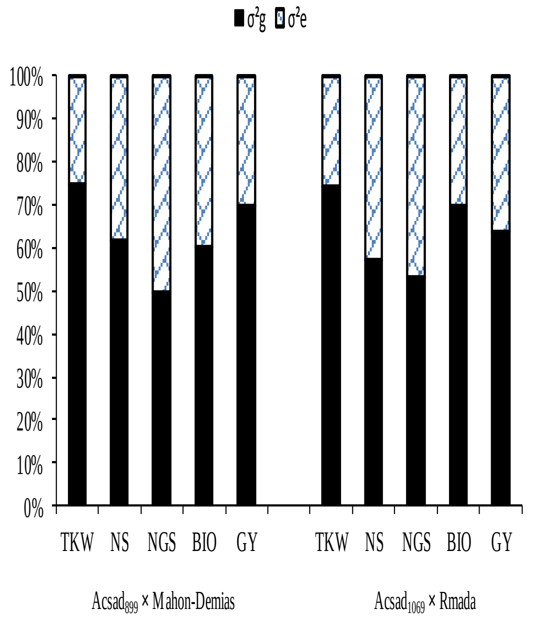

Figure 1. Relative contribution of the genetic and environmental variance components to the phenotypic variance for the measured traits in two bread wheat crosses.

3.3. Selection Differential, Expected Response to Selection and Expected Genetic Gain

The estimates of the selection differential for the studied characters ranged from 5.12 g for thousand-kernel weight in Acsad$_{899}$ × Mahon-Demias cross to 25.47 g for biomass per plant in Acsad$_{1069}$ × Rmada cross (Table 3). Positive selection differentials indicate the possibility of selecting genotypes with good performances. Knowledge of the expected response to selection and the consequent expected genetic gain are essential to identify the appropriate selection criteria (Acquaah, 2007). In Acsad$_{899}$ × Mahon-Demias cross, values of the expected response to selection for thousand-kernel weight, number of spikes per plant, number of grains per spike, above-ground biomass and grain yield were 3.83 g, 4.96 spikes, 8.50 grains per spike, 14.99 g and 8.04 g, respectively. Expressed as a percentage, the expected response to selection for grain yield took the highest value of 63.25%, suggesting an expected genetic gain, after the first cycle of selection, of 20.77 g. The lowest value, 10.58%, of the expected response to selection, expressed as percentage of the mean of base population, was recorded for thousand-kernel weight, leading to an expected genetic gain of 40.09 g.

In Acsad$_{1069}$ × Rmada cross, values of the expected response to selection for thousand-kernel weight, number of spikes per plant, number of grains per spike, above-ground biomass and grain yield were 4.51 g, 2.96 spikes, 9.08 grains per spike, 17.84 g and 7.21 g, respectively. The expected genetic gain values were 41.71, 10.96, 53.68, 48.21 and 21.02 for thousand-kernel weight, number of spikes per plant, number of grains per spike, above-ground biomass and grain yield, respectively (Table 3).

Table 3. Base population mean ($\bar{X}_o$), mean of the selected plants ($\bar{X}_s$), selection differential (S), expected response to selection (RS), expected response to selection expressed as percentage of the base population mean (%RS), and predicted gain genetic (PGG) for the studied characters of four populations (P$_1$, P$_2$, F$_1$ and F$_2$) derived from two bread wheat crosses.

Genetic component	Characters				
	TKW	NS	NGS	BIO	GY
Acsad$_{899}$ × Mahon-Demias					
$\bar{X}_o$	36.27	9.80	35.01	31.97	12.72
$\bar{X}_s$	41.38	17.83	52.06	56.83	24.26
S	5.12	8.03	17.04	24.87	11.54
RS	3.83	4.96	8.50	14.99	8.04
RS (%)	10.58	50.61	24.27	46.90	63.25
PGG	40.09	14.76	43.51	46.96	20.77
Acsad$_{1069}$ × Rmada					
$\bar{X}_o$	37.21	8.00	44.60	30.37	13.81
$\bar{X}_s$	43.28	13.17	61.71	55.83	25.07
S	6.07	5.17	17.11	25.47	11.26
RS	4.51	2.96	9.08	17.84	7.21
RS (%)	12.11	36.93	20.36	58.78	52.20
PGG	41.71	10.96	53.68	48.21	21.02

TKW: Thousand-kernel weight (g), NS: Number of spikes per plant, NGS: Number of grains per spike, BIO: Biomass per plant (g), GY: Grain yield per plant (g).

3.4. Heterosis, Potence Ratio and Inbreeding Depression

Heterosis over mid-parent and inbreeding depression percentage values in both crosses are presented in Figure 2 for the studied characters. Positive heterosis values for the number of spikes per plant, above-ground biomass and grain yield were observed in both crosses. A positive heterosis estimate was also recorded for the number of grains per spike in Acsad$_{1069}$ × Rmada cross. The heterosis values were low for grain yield and number of spikes but high for above ground biomass, in both crosses (Figure 2). Moreover, low and negative heterosis values were recorded for thousand-kernel weight in both crosses and for number of grains per spike in Acsad$_{899}$ × Mahon-Demias cross. Inbreeding depression was positive for number of spikes per plant, above-ground biomass and grain yield, and negative for thousand-kernel weight in both crosses (Figure 2). The maximum inbreeding effect was recorded for the number of spikes per plant in Acsad$_{899}$ × Mahon-Demias cross, while the minimum was exhibited by thousand-kernel weight in Acsad$_{1069}$ × Rmada cross. The positive estimates indicated that mean values of the F$_2$ generation were reduced compared to F$_1$ means. The degree of dominance of the various traits, presented as potence ratio, is reported in Table 4. Thousand-kernel weight potence ratio absolute value was greater than unity, in both crosses, suggesting over dominance. Over dominance acted in opposite directions, reducing this trait in Acsad$_{899}$ × Mahon-Demias and increasing it in Acsad$_{1069}$ × Rmada (Table 4). A partial dominance towards the higher parent was observed for the number of spikes per plant, biomass per plant and grain yield; and toward the lowest parent for number of grains per spike, in both crosses. Potence ratio absolute values of these traits were smaller than unity.

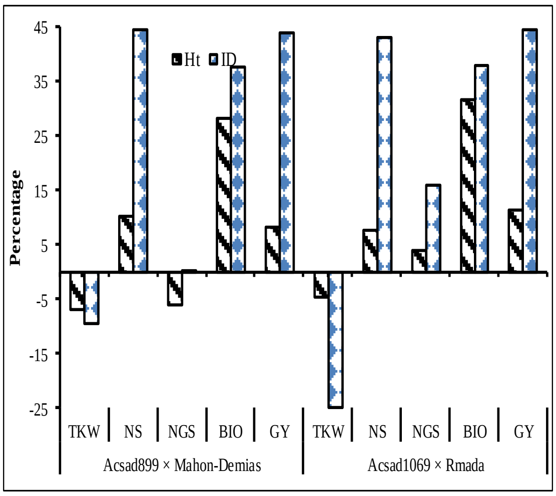

Figure 2. Percentage of heterosis (Ht) and inbreeding depression (ID) for the studied characters obtained in two bread wheat crosses.

Table 4. Potence ratio for the studied characters in two bread wheat crosses.

Characters	Potence ratio	
	Acsad$_{899}$ × Mahon-Demias	Acsad$_{1069}$ × Rmada
Thousand-kernel weight (g)	-2.75	2.24
Number of spikes per plant	0.60	0.36
Number of grains per spike	-0.33	-0.22
Above-ground biomass (g)	0.08	0.35
Grain yield per plant (g)	0.22	0.44

4. Discussion

Developing varieties resilient to moisture stress conditions and expressing high yield potential are an important objective in wheat breeding programs targeting arid and semi-arid regions. Various morphological, yield-related and physiological traits have been suggested as indicators for identifying drought tolerant genotypes (Richards *et al.,* 2002; Garcia del Moral *et al.,* 2003; Nouri *et al.,* 2011). The success of any plant breeding program depends on several factors including the amount of genetic variability, heritability and expected genetic gain of the trait under improvement. A higher amount of genetic variability accompanied by greater heritability and expected genetic gain will result in a significant progress through selection (Nouri *et al.,* 2011). To accumulate a desirable gene pool in improved germplasm, it is essential to understand the extent of genetic variation and the inheritance pattern of the metric traits in relation to the targeted environment for which varieties are to be developed (Farshadfar *et al.,* 2000). The results of the present study indicated a large phenotypic variation between parents and filial generations for the analyzed traits. Genetic components were greater than the environmental component of variance, suggesting negligible environmental effects. Several researchers, reviewed by Mohamed (2014), reported a sizeable variability in wheat cross populations for agronomic traits.

The results indicated that F$_1$'s were better than the best parents for spike number, above-ground biomass and grain yield, suggesting the presence of heterotic effects. Transgressive segregants for thousand-kernel weight and inbreeding depression for biomass, grain yield, grains per spike and spike number were observed in the F$_2$ generation. Koumber and El-Gammaal (2012) reported similar results. Broad sense heritability values were equal to or greater than 50% for the traits under study, suggesting possibilities for improvement through selection. Heritability values, observed in this study, are of the same magnitude as those reported by Khan *et al.* (2007) and Khaled (2013). Knowledge of the heritability is important to breeders, because it measures the degree to which a character may be transmitted from parents to offspring and it indicates the extent to which the improvement is possible through selection (Acquaah, 2007). The studied traits are controlled by a relatively small number of genes, suggesting that few selection cycles would be necessary to obtain the required accumulation of the favorable alleles controlling them. The expected response to selection, expressed as a percentage of the base population mean, varied from 10.58% for thousand-kernel weight to 63.25% for grain yield.

Farshadfar *et al.* (2001) mentioned that moderate to high estimates of the expected response to selection suggest that the early selection could be effective as a strategy to improve the traits under study, whereas the delayed selection would be more effective to improve characters which exhibited a low expected response to selection values. Results indicated that over dominant inheritance was involved in thousand-kernel weight control, while partial dominance was involved in the genetic control of the other traits. Both additive and non-additive gene actions were involved in the expression of most agronomic characters (Hannachi *et al.,* 2013). Mohamed (2014) reported over dominance in the inheritance of these traits in two wheat crosses. Rashid *et al.* (2007) indicated that the grain yield was controlled by additive gene effects. Hassan *et al.* (2007) and Akhtar and Chowdhry (2006) reported that a partial dominance was involved in biomass, spike number and thousand-kernel weight.

The results suggested, based on h^2_{bs}, expected response to selection which expressed the significance of additive gene effects, that the early selection could be effective to improve the number of spikes, above ground biomass, grain yield, and the number of grains per spike while delayed selection could be applied to improve thousand-kernel weight. In fact, a sizeable contribution of the dominance effect suggests postponing the selection of the character under improvement to advanced generations when a sufficient reduction of the dominance variance component is reached. However, in the presence of high dominance effect it is still possible to select superior plants in the progenies of a cross for a trait of interest.

5. Conclusion

In the present study, different characters were evaluated by estimating various genetic parameters in segregating and non-segregating generations in two bread wheat crosses under semi-arid environment. The results indicated the presence of desirable transgressors, in both crosses, for a number of spikes per plant; desirable transgressors for thousand-kernel weight, above-ground biomass and grain yield, and undesirable transgressors for number of grains per spike in Acsad$_{1069}$ × Rmada cross. Estimates of broad sense heritability took intermediate to high values for all characters under study, expressing the significance of additive gene effects and indicating possibilities for improvement through selection. The expected response to selection varied among traits and was of a similar magnitude in both crosses. Over dominance was observed in the expression of thousand-kernel weight, and partial dominance was observed for a number of spikes, above-ground biomass, grain yield, and number of grains per spike, in both crosses. The results suggested that the early selection could be effective to improve the number of spikes, above-ground biomass, grain yield, and number of grains per spike while delayed selection could be applied to improve thousand-kernel weight.

References

Acquaah G. 2007. **Principals of Plant Genetics and Breeding**. Blackwell Publishing, Oxford, UK.

Akhtar N and Chowdhry MA. 2006. Genetic analysis of yield and some other quantitative traits in bread wheat. *Inter J Agricul Biol*., **4**: 523–527.

Beche E, Da Silva CL, Pagliosa ES, Capelin MZ, Franke J, Matei G and Benin G. 2013. Hybrid performance and heterosis in early segregant populations of Brazilian spring wheat. *Australian J Crop Sci.*, **7(1)**: 51–57.

Blum A. 1996. Crop responses to drought and the interpretation of adaptation. *Plant Growth Regulation*, **20**: 135-148.

Bray EA. 2002. Classification of genes differentially expressed during water-deficit stress in *Arabidopsis thaliana*: an analysis using microarray and differential expression data. *Ann Botany,* **89**: 803–811.

Burton GW. 1951. Quantitative inheritance in pearl millet (*Pennisetum glaucum*). *Agronomy J.,* **43**: 409–417.

Cattivelli L, Rizza F, Badeck FW, Mazzucotelli E, Mastrangelo AM, Francia E, Marè C, Tondelli A and Stanca AM. 2008. Drought tolerance improvement in crop plants: an integrated view from breeding to genomics. *Field Crops Res.*, **105 (1-2)**: 1–14.

Chennafi H, Aïdaoui A, Bouzerzour H and Saci A. 2006. Yield response of durum wheat (*Triticum durum* Desf.) cultivar Waha to deficit irrigation under semiarid growth conditions. *Asian J Plant Sci.,* **5**: 854–860.

Cruz CD. 2013. Genes: a software package for analysis in experimental statistics. *Acta Sci Agronomica,* **35**: 271–276.

Cruz CD, Regazzi AJ and Carneiro PCS. 2012. **Modelos Biométricos Aplicadosao Melhoramento Genético** - ISBN 9788572694339. 4th ed. UFV, Viçosa.

Falconer DS and Mackay TFC. 1996. **Introduction to Quantitative Genetics**. Longman, Essex, 4th ed. Edition, UK.

Farshadfar E, Farshadfar M and Sutka J. 2000. Combining ability analysis of drought tolerance in wheat over different water regimes. *Acta Agronomica Hungarica*, **48**: 353–361.

Farshadfar E, Ghandha M, Zahravi M and Sutka J. 2001. Generation mean analysis of drought tolerance in wheat (*Triticum aestivum* L.). *Acta Agronomica Hungarica*, **49**: 59–66.

Fellahi Z, Hannachi A, Bouzerzour H and Boutekrabt A. 2013. Line × tester mating design analysis for grain yield and yield related traits in bread wheat (*Triticum aestivum* L.). *Inter J Agronomy*, **2013**, Article ID 201851, 9 p.

Fonsecca S and Patterson FL. 1968. Hybrid vigour in seven-parent diallel cross in common wheat (*T. aestivum* L.). *Crop Sci*., **2**: 85–88.

Garcia del Moral LF, Rharrabti Y, Villegas D and Royo C. 2003. Evaluation of grain yield and its components in durum wheat under Mediterranean conditions: an ontogenic approach. *Agronomy J*., **95**: 266–274.

Gowda M, Kling C, Würschum T, Liu W, Maurer HP, Hahn V and Reif JC. 2010. Hybrid breeding in durum wheat: heterosis and combining ability. *Crop Sci*., **50**: 2224–2230.

Hannachi A, Fellahi Z, Bouzerzour H and Boutekrabt A. 2013. Diallel-cross analysis of grain yield and stress tolerance-related traits under semi-arid conditions in durum wheat (*Triticum durum* Desf.). *Electronic J Plant Breeding*, **4 (1)**: 1027–1033.

Hassan G, Fida M, Shah A and Khalil I. 2007. Combining ability in the F_1 generation of diallele cross for yield and yield components in wheat. *Sarhad J of Agricul.,* **23**: 56–72

Kaur V and Behl RK. 2010. Grain yield in wheat as affected by short periods of high temperature, drought and their interaction during pre- and post- anthesis stages. *Cereal Res Communications*, **38**: 514–520.

Khaled MAI. 2013. Analysis of yield and yield components in two bread wheat crosses under water stress conditions. *Egyptian J Agricul Res.*, **91(4)**: 1489–1501.

Khan I, Khalil IH and Nasir-ud-Din. 2007. Genetic parameters for yield traits in wheat under irrigated and rainfed environments. *Sarhad J Agricul.*, **23(4)**: 973–980.

Koumber RM and El-Gammaal AA. 2012. Inheritance and gene action for yield and its attributes in three bread wheat crosses (*Triticum aestivum* L.). *World J Agricul Sci.,* **8(2)**: 156–162.

Mohamed NEM. 2014. Genetic control for some traits using generation mean analysis in bread wheat (*Triticum aestivum* L.). *Inter J Plant Soil Sci.*, **3(9)**: 1055–1068.

Mullet JE and Whitsitt MS. 1996. Plant cellular responses to water deficit. *Plant Grow Regulation*, **20**: 119–124.

Nezhadahmadi A, Prodhan ZH and Faruq G. 2013. Drought tolerance in wheat. *Sci World J.*, **2013**, Article ID 610721, 12 p.

Noorka IR., Rehman S, Haidry JR, Khaliq I, Tabassam S and Din M. 2009. Effect of water stress on physico-chemical properties of wheat (*Triticum aestivum* L.). *Pak J Botany*, **41(6)**: 2917–24.

Nouri A, Etminan AJ, Teixeira da Silva JA and Mohammadi R. 2011. Assessment of yield, yield-related traits and drought tolerance of durum wheat genotypes (*Triticum turgidum* var. *Durum* Desf.). *Australian J Crop Sci.,* **5**: 8–16.

Peter FC and Frey KJ. 1966. Genotypic correlations, dominance and heritability of quantitative characters in oats. *Crop Sci*,, **6**: 259–262.

Rashid M, Cheema AA and Ashraf M. 2007. Line x tester analysis in basmati rice. *Pak J Botany*, **39**: 203–2042.

Richards RA, Rebetzke GJ, Condon AG and Van Herwaarden AF. 2002. Breeding opportunities for increasing the efficiency ofwater use and crop yield in temperate cereals. *Crop Sci.*, **42**: 111–121.